

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:03:30 ; Search time 1496.56 Seconds
(without alignments)
2929.570 Million cell updates/sec

Title: US-09-540-235-1
Perfect score: 408
Sequence: 1 accgcgcgtcgttcgaatta.....acatccatcaatgttgtta 408

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 11351937 segs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estda:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	133.8	32.8	454	10	BE636128 SNEST4A15
2	133.8	32.8	489	10	AL381742 MTRC02F09
3	133.2	32.6	637	13	AQ963432 LERGI927R
4	131.6	32.3	649	13	AQ963431 LERGI927R
5	130.4	32.0	409	11	BF052600 EST437830
6	130.4	32.0	487	11	BE924162 EST427931
7	130.4	32.0	612	11	BI178667 EST519612
8	129	31.6	340	10	AI164427 A061P34U
9	129	31.6	467	11	BF517187 NXSL_011
10	128.8	31.6	477	10	AI164301 A058P78u
11	128.4	31.5	471	10	AW289566 NXNV00260
12	127.6	31.3	389	10	AL388757 MTRC50E10

13	127	31.1	349	10	AA841097
14	126.4	31.0	525	10	A1490797
15	126.4	31.0	527	10	A1772648
16	126.4	31.0	534	10	A1490076
17	126.4	31.0	538	10	AM040995
18	126.4	31.0	564	10	BE450458
19	126.4	31.0	566	11	BG132272
20	126.4	31.0	595	11	A1482959
21	126.4	31.0	609	11	BG123744
22	126.4	31.0	625	10	AM220037
23	126.4	31.0	744	11	BG123632
24	126	30.9	396	11	BG627962
25	126	30.9	439	11	BG643800
26	126	30.9	477	10	AM037370
27	126	30.9	489	10	A1778920
28	126	30.9	535	10	A1775702
29	126	30.9	560	11	BG134065
30	126	30.9	601	11	B1210092
31	126	30.9	604	11	B1209065
32	126	30.9	621	11	BG127514
33	126	30.9	627	11	BG130661
34	126	30.9	648	11	BG129875
35	125.4	30.7	379	10	AM290853
36	125.2	30.7	401	11	BF610389
37	124.8	30.6	531	10	A1484130
38	124.6	30.5	553	11	B1179552
39	124.6	30.5	607	10	AM906936
40	124.6	30.5	615	11	BG598740
41	124.6	30.5	616	11	BG600593
42	124.6	30.5	629	11	BG598622
43	124.2	30.4	543	11	BG817601
44	123.2	30.2	441	10	A1778533
45	122.8	30.1	667	11	BF707483

ALIGNMENTS

RESULT 1
LOCUS BE636128 454 bp mRNA EST 25-AUG-2000
DEFINITION SNEST4A15I07.y1 csn 1 s neurona invitro mezoite cDNA Sarcocystis
neurona cDNA 5' similar to TR:082579 082579 RIBOSOMAL PROTEIN L26
; mRNA sequence.

ACCESSION BE636128 GI:9918815
VERSION BE636128.1
KEYWORDS EST.
SOURCE Sarcocystis neurona.
ORGANISM Sarcocystis neurona
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Sarcocystis.
1 (bases 1 to 454)

REFERENCE
AUTHORS Howe,D.K., Stamper,S., Tang,K., Sibley,L.D., Clifton,S., Marra,M.,
Hillier,L., Pape,D., Martin,J., Wylie,T., Theisling,B., Bowers,Y.,
Gibbons,M., Ritter,E., McCann,R., Bilstain,A., Benne,J., Schmitt,
A., Ronko,I., Tsagareishvili,R., Fedele,M., Belaygorod,L.,
Franklin,C., Carr,L.M., Grow,A., Maguire,L., Wadkins,J., Ritchey,J.,
Waterston,R. and Wilson,R.

Sarcocystis neurona EST project
Contact: Daniel K. Howe
Unpublished (2000)
Sarcocystis neurona EST project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Contact Daniel K. Howe (dkhowe2@pop.uky.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: 40RP from Gibco
High quality sequence stop: 401.
Location/Qualifiers
1. 454

TITLE
JOURNAL
COMMENT

FEATURES
source

KEYWORDS	GSS.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 637)
REFERENCE AUTHORS	Buell, C.R., Lin, X., Pat, G., Barnstead, M., Bowman, C., Utterbach, T., Reidlyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
TITLE	Unpublished (2000)
JOURNAL	Contact: Xiaoying Lin The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: ateflgr.org
COMMENT	For additional information, see http://www.tigr.org/tdb/at/at.html Seq primer: TR Class: Shotgun.

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BASE COUNT      208 a      144 c      131 g      154 t
ORIGIN
/note="Organ: Leaf; Vector: pUC19JF; Total genomic DNA was
sheared to 0.4-0.7 kbp before ligation."

```

Query Match	32.6%	Score 133.2	DB 13	Length 637
Best Local Similarity	63.4%	Pred. No. 3.1e-27		
Matches	204	Conservative	0	Mismatches 118; Indels 0; Gaps 0;
QY	87	tcagtcgcacatgaatctccaaagttgatctgtctctagaagaagcagaagaagca	146	
Db	312	TCGGCGGGCATGAAGTTCAATCCGGGTGTGACCTCTTCTCGCCGGAGAACAGAGCTT	371	
QY	147	tacttcaagcaccatctctgtacgacgaatactcaatgaatgacacctgtccaaggaa	206	
Db	372	CACCTTCACAGCCTCTTCAAGCGCTGAGGCGCTTCATGATGAGCTCCGCCGTTATCCAAGAC	431	
QY	207	ctacgtacgaataaagaagttcttcttactatctgcaaaagaagaagaatcata	266	
Db	432	CTCCGTAACAAATTAACAAGCTGAGATCCATGCCGATTCGTAAAGACGAGCAAGTTC	491	
QY	267	gttcgcggaagcttccaagagtagaagaagaagttacaacgttgttatcgaaagaatat	326	
Db	492	GTTCCTGGGACGTTCAAGGGAAGAGAAAGGATGATCCAGGTATATCGCCGCAAGTGG	551	
QY	327	cgaalacatcogagaagatgaccagaagaanaagcgaatggaaatgacttacctgtgga	386	
Db	552	GTCATTCAATCGAGAGAAATCAAGGGAGAAAGTCACAGCAACCAAGGTCAACCTCGGA	611	
QY	387	ataactcatcatcaatgttgtta	408	
Db	612	GTCATGCTTCGAATGTGATGA	633	

RESULT	4			
AO963431/c				
LOCUS		649 bp	DNA	28-JAN-2000
DEFINITION	AO963431	LERG1922F LER6 Arabidopsis thaliana genomic clone LERG192, DNA		
ACCESSION	sequence.			
VERSION	AO963431			
KEYWORDS	AO963431.1	GI:6791132		
SOURCE	GSS.			
	thale cress.			

ORGANISM Arabidopsis thaliana
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots:
Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis.
1 (baes 1 to 649)
Buell, C., Lin, Y., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
Feildblum, T., Liang, F., Cerasy, T., and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atetigr.org
For additional information, see <http://www.tigr.org/tdb/at/at.html>
Seq primer: TF
Class: Sholgun.

```

BASE COUNT      156 a      143 c      149 g      201 t
ORIGIN
/Note=Organ: Leaf; Vector: pUC19JK; Total genomic DNA was
sheared to 0.4-0.7 kbp before ligation."

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	Query Match	32.3%;	Score 131.6;	DB 13;	Length 649;	
	Best Local Similarity	63.0%;	Pred. No. 8.7e-27;			
	Matches 203; Conservative	0;	Mismatches 119;	Indels 0;	Gaps 0;	
QY	87	tcaatcgccataagaattaccaaagtlgtatcgtctgctatagaagaacgaqanaa	146			
Db	383	TGCGGGCGGATGAAGTTCAATCCGGGTGTGACCTTTCGCCGGAATAACAGGAGCT	324			
QY	147	tacttccaagacacatcttcgttagcacgaatactcatgaqtgcaccccttgcgaaggaa	205			
Db	323	CACCTTCACAGCTCCTTCMAAGCGTGAGCGGCTTCATCAGACTCGCCSTATTCCAAGAC	264			
QY	207	ctaagtgaagaatacagtggttcgtcttaccttactcttgaagaagaagaagtatacata	266			
Db	263	CTCCGTAAACAATATCMACGTCAGATTCATGCCTGAATGTAAGAAGAGTCCAACTT	204			
QY	267	gttcgcyagagctttcaaaggtfagaagaagaatttaacaacgttgtatcgaagaataat	326			
Db	203	GTTGCGTGGAGCTTCAAGGCGAAGAGGAAAGGTGATGCGAGGTGTATCGCCCGCAAGTGG	144			
QY	327	cgaatatacatacgsaagagtgaccagaagaaaacgaaatgaaatgaaatgtaactcttggaa	386			
Db	143	GTCATTCACATCGAGAAATCACAAAGGAGAAACTCAACGGAACCGCGTCAACGTGGGA	84			
QY	387	atacatccatcaatgtgttta 408				
Db	83	GTCATGCTTCGAATGTGATGA 62				

RESULT	5
BF052600	
LOCUS	BF052600
DEFINITION	BF052600 409 bp mRNA
ACCESSION	EST47830 potato leaves and petioles Solanum tuberosum cDNA clone
VERSION	CS832602 5' sequence, mRNA sequence.
KEYWORDS	BF052600.1 GI:10806496
SOURCE	EST.
ORGANISM	potato.
	Solanum tuberosum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

REFERENCE 1 (bases 1 to 612)
 AUTHORS van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,
 Chieningo, A., Bougri, O., Buell, C.R., Roming, C., Tanksley, S. and
 Baker, B.
 TITLE Generation of ESTs from in vitro grown microtubers
 JOURNAL Unpublished (2001)
 COMMENT Contact: Cathy Roming
 The Institute for Genomic Research
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdnaresgen.com
 Seq primer: M13P-R.
 FEATURES
 source
 Location/Qualifiers
 1..612
 /organism="Solanum tuberosum"
 /cultivar="Bintje"
 /db_xref="taxon:4113"
 /clone_lib="EST589"
 /clone_1lb="cSTE"
 /tissue_type="axillary buds of stem explants; growing
 sink-tubers"
 /dev_stage="7, 8 and 10 days"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; Tissue supplied by Christian Bachem and Rich-
 Visser (Department of Plant Breeding, Wageningen
 University, The Netherlands). The cSTRA libraries will
 attempt to capture the induction and initiation/initial
 growth of the tuber in an in vitro system as described in
 Bachem et al. (Plant Journal, 1996). Small microtubers
 develop from axillary buds attached to stem explants when
 placed on a high sucrose medium (10%). Visible
 morphological changes occur synchronously at day five in
 the axillary buds. The first library, cSTRA (1-20) consists
 of axillary buds harvested on days 1-3. This targets
 those genes involved in induction of the microtubers. The
 following libraries, cSTRA (21-40) and cSTRA (41-60),
 capture genes involved in tuber initiation and outgrowth.
 This library is noted as p3 in Tanksley lab notebooks."
 BASE COUNT 171 a 101 c 152 g 188 t
 ORIGIN

Query Match 32.0%; Score 130.4; DB 11; Length 612;
 Best Local Similarity 62.7%; Pred. No. 1.9e-26;
 Matches 203; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

84 gtatcagtcgcgaatattccaaagtgtatcgtctagaagaacagagga 143
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 17 GTTTCGACACATGATACATCCAGAGATTCTCTCCGCGTAAGAGCAAG 76
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 144 gcatccttcaagcacatctctctgtacgcgaatactatcagtgacccctgtccaag 203
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 77 GCCCATTTTCACTGCTCCATCAAGCGTTCGACGGGTGTGATGAGCGACCCCTTTCATCT 136
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 204 gaactagtagaagaatgaagcttcgtcttactatctgaagaagaagacgaatc 263
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 137 GAGTTACCTACCAAGTACACGTACATCTATCCCGGTGAAGAAAAGATGAGATTCAA 196
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 264 atagtcgcgaagcttcaaggtgagagaagaatcttacaagctgttctcgaaga 323
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 197 GTAGTAAGAGAGACCTACCAAGGCGCGTAAGGAAATGTTATGCAAGTTCACCGTAAGAAA 256
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 324 tatcgatatacatcgagagagtgaccagagaaacgaatggaatgactgtacccgtg 383
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 257 TGGGTGATTCACATTCAGCGGTATACAGAGAAAGTTATGATGATCTACTGTTAATGTT 316
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 384 ggaatacatcatatgttgtt 407
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 317 GGTATTAATCATCTAAGGTTGTT 340

LOCUS A1164427 340 bp mRNA EST 03-DEC-1998
 DEFINITION A061P34U Hybrid aspen plasmid library Populus tremula x Populus
 tremuloides cDNA 5', mRNA sequence.
 ACCESSION A1164427
 VERSION A1164427.1 GI:3855712
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides.
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
 1 (bases 1 to 340)
 REFERENCE
 AUTHORS Sterky, F., Regan, S., Karlsson, J., Hertberg, M., Rohde, A., Holmberg
 'A., Amin, B., Bhalerao, R., Larsson, M., Villarroel, R., Van Montagu
 'M., Sandberg, G., Olsson, O., Teerl, T.T., Boerjan, W., Gustafsson, P.,
 Uhlen, M., Sundberg, B. and Lundberg, J.
 Gene discovery in the wood-forming tissues of poplar: Analysis of
 5,692 expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
 99007314
 COMMENT Contact: Sterky F
 Department of Biotechnology
 Royal Institute of Technology (KTH)
 Teknikringen 34, S-100 44 STOCKHOLM, Sweden
 Tel: +46 8 790 8287
 Fax: +46 8 24 54 52
 Email: fredrik@biochem.kth.se
 PCR Primers
 FORWARD: AAGGGGATGCTGTCGACGGCG
 BACKWARD: GCTCCGGCTGCTGATGCTGCG
 Seq primer: CGTTGTAACGACGGCCAG
 High quality sequence stop: 340.
 Location/Qualifiers
 1..340
 /organism="Populus tremula x Populus tremuloides"
 /db_xref="taxon:47664"
 /clone_1lb="Hybrid aspen plasmid library"
 /tissue_type="Cambial region"
 /dev_stage="1.5 m actively growing tree"
 /lab_host="E.coli"
 /note="Vector: pBluescript SK(-); Site_1: SalI; Site_2: NotI;
 Cambial region tissues, including developing xylem, the
 meristematic cambial zone and the developing and mature
 phloem, was harvested from 1.5 m actively growing trees.
 cDNA was prepared and cloned into Lambda gt10a. DNA was
 isolated and subcloned into pBluescript SK using SalI and
 NotI restriction enzymes."
 BASE COUNT 98 a 82 c 88 g 72 t
 ORIGIN

Query Match 31.6%; Score 129; DB 10; Length 340;
 Best Local Similarity 65.0%; Pred. No. 4.2e-26;
 Matches 206; Conservative 0; Mismatches 110; Indels 1; Gaps 1;

92 cgcataaagattccaaggtgtatcgtctcgtctagaagaacagagaagcactact 151
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2 CACGATCAATATACACCCAGAGATCTCTCTCCCGAAGAACCGTAAGGCCCACTT 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 152 tcaagcacatctctctgtacgcgaatactatcagtgacccctgtccaagaactg 211
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 62 CTCGGCGCATCTCTCGTGGTGTGATCTCATGACGACACCACTTCCACGCACTCG 121
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 212 taagaataacagcgtctcgtcttactatctgaaagaagaagacgaatcatagttcg 271
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 122 TCAGAAATACACAGTGATGATCCATCCGAAAGACGATGAGATCAAGTTGTTG 181
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 272 cggagcttcaaggtgagagaagaattacaagctgttctcgaagaataatcgat 331
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 182 TGGGACATACCAAGGAGGAGGAGGAGGTTTCAAGGTTTAAAGGAAATGGGATAT 241
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 332 acatatcgagagagtgaccagagaaacgaatggaatgactgtactgttggaataca 391
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
 A1164427

Db 242 TCATGTCGAGAGATTACAAAGGAAAGTTAATGATCCACTGTATAC GTGGCAATTAA 300
 QY 392 tccatcaatcgttgta 408
 Db 301 CCTTCGAAGTGCTGA 317

RESULT 9
 BF517187 467 bp mRNA EST 08-DEC-2000
 LOCUS BF517187
 DEFINITION NXS1_011.D12.F NXS1 (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
 clone NXS1_011.D12.5', mRNA sequence.
 ACCESSION BF517187
 VERSION BF517187.1 GI:11604790
 KEYWORDS EST.
 SOURCE lobliolly pine.
 ORGANISM Pinus taeda
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 Sederoff, R.
 1 (bases 1 to 467)
 TITLE Molecular Basis of Wood Formation in the Pine Megagenome
 JOURNAL Unpublished (2000)
 COMMENT Contact: Johnson, Arthur
 North Carolina State University
 Tel: 919 515 7800
 Fax: 919 515 7801
 Email: a.johnson@unity.ncsu.edu
 Seq primer: T3.

FEATURES
 SOURCE
 1..467
 Location/Qualifiers
 /organism="Pinus taeda"
 /strain="Coastal plain lobliolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXS1_011.D12"
 /clone_lib="NXS1 (Nsf Xylem Side wood Inclined)"
 /tissue_type="Xylem"
 /cell_type="Side"
 /dev_stage="Juvenile"
 /lab_host="XLI-Blue"
 /note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
 ; The library is from early (spring) wood, taken from
 three six-year old trees (three different genotypes), in
 the juvenile phase. These trees were induced to form side
 wood by bending to a 45 degree angle and tying them to the
 ground. Differentiating xylem was harvested from the sides
 of the inclined stems, and a mixture of all three
 genotypes was used for the library. Oligo-dT primed cDNA
 was directionally cloned into the EcoRI-XhoI Bluescript SK
 vector arms. NOTE: The sequences contain a 'cDNA adapter'
 between the EcoRI site and the start of the EST. The
 adapter sequence is 'AATTCGACGAC'."

BASE COUNT 140 a 78 c 121 g 111 t 17 others

ORIGIN
 Query Match 31.6%; Score 129; DB 11; Length 467;
 Best Local Similarity 62.4%; Pred. No. 4.5e-26;
 Matches 201; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 86 atagtcgcatagaatcattccaaagttgatcgtctcgtctagaagaagaagcagaagc 145
 Db 22 AACCTTCGATATGAATACATCCAGAGTCACTAGCTCTAGAGAAAGAGCCGAGAGC 81

QY 146 ataacttcaagcacaactcttcgtacgaagaatactcagatgcaccccttgcagaaga 205
 Db 82 ACATTTTACTGCCCATCTAGTCTCCGGCGTATTGATGAGTGCCTCCCTTTCTCTA 141

QY 206 actacgtagaanaacagcgtctcgtcttactcattcgaagaagaagaatcatc 265
 Db 142 TCTGAGGAACAACTATTAATGTTGTTCTATCCCAATTAGAAAGATGATGAAGTTAGGT 201

QY 266 agtcgcgagcttcaaggttagagaaggaagttacaagctgttactgaaagaata 325

Db 202 TGTGCGAGAGACTTCACAGGAGAGAGCGCAAGTTGTTCAAGTTTATCCGAAGAACTG 261
 QY 326 tcggatcacatcagagagatgaccagagaagaacgagatggaatgactgaccggtg 385
 Db 262 GGTCAATCCATGTTGAGCGCATCTACGCGAGAAAGTCAATGATGATCAATGTTGG 321

QY 386 aatacatccatcattatgtgtt 407
 Db 322 TGTTCACCATCGAAGCTTCTT 343

RESULT 10
 A1164301 477 bp mRNA EST 03-DEC-1998
 LOCUS A1164301
 DEFINITION A058p78u Hybrid aspen plasmid library Populus tremula x Populus
 tremuloides cDNA 5', mRNA sequence.
 ACCESSION A1164301
 VERSION A1164301.1 GI:3855586
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides.
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
 Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
 Sterky, F., Regan, S., Karlsson, J., Hertzberg, M., Rohde, A., Holmberg
 1 (bases 1 to 477)
 TITLE
 JOURNAL
 MEDLINE
 COMMENT Contact: Sterky F
 Department of Biotechnology
 Royal Institute of Technology (KTH)
 Teknikringen 34, S-100 44 STOCKHOLM, Sweden
 Tel: +46 8 790 8287
 Fax: +46 8 24 54 52
 Email: fredrik@biochem.kth.se
 PCR Primers
 FORWARD: AAGGGGAGATGCTCTCAGGCG
 BACKWARD: GCTTCGGCTGTATGTGTG
 Seq primer: CGTTGAAACGACGGCCAG
 High quality sequence stop: 477.
 Location/Qualifiers
 1..477
 /organism="Populus tremula x Populus tremuloides"
 /db_xref="taxon:47664"
 /clone_lib="Hybrid aspen plasmid library"
 /tissue_type="Cambial region"
 /dev_stage="1.5 m actively growing tree"
 /lab_host="E.coli"
 /note="Vector: Bluescript SK; Site_1: SalI; Site_2: NotI;
 Cambial region tissues, including developing xylem, the
 meristematic cambial zone and the developing and mature
 phloem, was harvested from 1.5 m actively growing trees.
 cDNA was prepared and cloned into lambda gt22a. DNA was
 isolated and subcloned into pBluescript SK using SalI and
 NotI restriction enzymes."

BASE COUNT 130 a 107 c 130 g 107 t 3 others

ORIGIN
 Query Match 31.6%; Score 128.8; DB 10; Length 477;
 Best Local Similarity 62.8%; Pred. No. 5.1e-26;
 Matches 199; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 92 cgcactgaagattccaaagttgatcgtctcgtctagaagaagcagaggaagcactct 151
 Db 8 CACAAATGAAGNACCAAGAGTCTCTCTCCGCGCGGAAGAACGTAAGGCCACTT 67

RESULT	11
LOCUS	AM289566
DEFINITION	AM289566 471 bp mRNA
ACCESSION	NK0V002G02F Nsf xylem Normal wood Vertical Pinus taeda cDNA clone
VERSION	AM289566 5', mRNA sequence.
KEYWORDS	AM289566 GI:6696202
SOURCE	EST.
ORGANISM	loblolly pine. Pinus taeda

REFERENCE	TITLE	JOURNAL	AUTHORS	COMMENT
1. (pages 1 to 471)	Molecular Basis of Wood Formation in the Pine Megagenome	unpublished (2000)	Seideroff, R.	
		Contact: Johnson, Arthur		

North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES	Location/Qualifiers
source	1. .471

BASE COUNT	142 a	78 c	130 g	108 t	13 others
ORIGIN					

Query Match	31.5%;	Score 128.4;	DB 10;	Length 471
Best Local Similarity	62.4%;	Pred No 6	6e-26.	

Matches	201;	Conservative	0;	Mismatches	121;	Indels	0;	Gaps	0;
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OY 86 atcagtcgccatgaaagtattccaaagttgtatcgctcagaagaagcagagaaagc 145
 | | | | | | | | | | | | | | | | | | |
Db 55 AACCTTCGATATGAAGTACCAATCCAAAGAGTCAGTAGCCTTAGGAGAAGAGCGCGGAGGC 114

QY 146 atacttcaagcaccatcttctgtacagcgaatactcatgtatgacccctgtccaagga 205

Db 115 ACATTCTACTGCCCATCTAGTGTCCGCGATTTTGATGAGTGTCCGCTTCTCTGA 174

206 actacgtacgaaatacagcgcttcgtcttacctatlcgaaagaagacgaagtatcat 265

Db 175 TCTGAGGACCAAGTATATGTTCTGTTCTATCCCAATTAGAAAGATGATGACGTTACAGT 234

QY 266 agtcgcggagccttcacagggtagaagaagaaagtltaacaagctgtgtltaacgaagaata 325
Db 235 TATGGAGGAACGTTTCAAGGGAAGAGAGGCGCAAGTTGTTCAAGTTTATGTGAAGAG 294
QY 326 tcggatataatcgagagagtgaccacgaagaaagcgaatgaaabactgtctctgtgg 385
Db 295 GGTCTTCATCTTTAAGGCGCAATTACTCGGAGAAAGTCATCGTACCAACTGTAAAGTTGG 354
QY 386 aatacatcatcattatgtgt 407
Db 355 TGTTCACCCATCGAAGGTTGTT 376

RESULT	12			
LOCUS	AL388757			
DEFINITION	AL388757	389 bp	mRNA	EST
ACCESSION	MEM50E10F1	mtbc	Medicago truncatula	cdna clone MTEC50E10 T3, mRNA
VERSION	AL388757			
KEYWORDS	AL388757.1	GI:9688508		
SOURCE	EST.			
	barrel medic.			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
(pages 1 to 389)	Journet, E.P., Crespeau, H., van Tuinen, D., Gouzy, T., Tallon, O., Niebel, A., Carreau, V., Chataigner, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.	Medicago truncatula ESTs from endomycorrhizal roots	Unpublished (2000)	Contact: Genoscope

Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: segreff@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamais and Etienne-Pascal Jounel, Laboratoire de
Biologie Moléculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
M-est@toulouse.inra.fr Website :
<http://sequence.toulouse.inra.fr/Mtruncatula.html>).

FEATURES	Location/Qualifiers
source	1. .389

```

/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBC50E10"
/clone_lib="MCBC"
/tissue_type="arbuscular mycorrhiza"
/dev_stage="harvested 3 weeks post inoculation with Glomus"
/intradermics"

```

note="Vector: pBluescript PSK, Site.1: EcoRI, Site.2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Eppisettes soil: 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate IP48). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Clontack Gold packaging extracts. Plasmids containing cDNAs were mass-excised from phage stocks using ExSactI helper phage and propagated in SOLr cells. Clone ordering and sequencing was performed by the Centre National de Séquençage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT	129 a	70 c	88 g	102 t
ORIGIN				

FEATURES
source
Location/Qualifiers
1. .525
/organism="Lycopersicon esculentum"
/cultivar="TA96"
/db_xref="taxon:4081"
/clone="CLEB36"
/clone_lib="tomato shoot, Cornell"
/tissue_type="shoot meristem"
/dev_stage="8 week old plants"
/lab_host="X10LR"
/note="Vector: pK-CMV; Site_1: EcoRI; Site_2: XhoI; CLER - tomato shoot Meristem EST Library. Oligo-dT primed cDNA library made from tomato vegetative shoots including meristems and small expanding leaves."
BASE COUNT 153 a 104 c 135 g 133 t
ORIGIN

Query Match 31.0%; Score 126.4; DB 10; Length 525;
Best Local Similarity 62.8%; Pred. No. 2.5e-25;
Matches 196; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 96 atgaagatcccaagtgatcgtcgtcgaagaagaagaagaacatacttca 155
Db 18 ATGAAGTACAAATCCAGAGATCTCTCCGCGGAAGAGCAGGCTCATTTACG 77
Qy 156 gcaccatctctgtagcagaatactcagtagtcaccctgtccaaaggaactcag 215
Db 78 GCGCCTTCAAGTGGCGCGCGATTTTAATGACCGCACCTTATGTCGAGTTACGTGA 137
Qy 216 aaatacagcgttcgtcttaccatcgaagaagaagaagaatcatagtcgcgga 275
Db 138 AAGTACACGTAAGATCTATGCCGTGAGAAAGATGACGAAGTTGTCGTTGCGGA 197
Qy 276 gcttcaaggtagaagaagaagaatcacaacgtgtatcgaagaagaatcagatcat 335
Db 198 ACTTACAAAGGCGCGTACGAGGAAGTTGTTCAAGTGTACCTAAGAAATGGTGATCCAC 257
Qy 336 atcgagaagtagcagcagaagaagaagaatgaatgaatgaatgaatgaatcaca 395
Db 258 ATTGAACGTATACACGAGAGAGTCATGATCTACTGTGAACGTTGGATTCATCCT 317
Qy 396 tctaattggt 407
Db 318 TCGAAGTTGTT 329

RESULT 15
AI772648 527 bp mRNA EST 18-MAY-2001
LOCUS EST253748 tomato resistant, Cornell Lycopersicon esculentum cDNA
DEFINITION
ACCESSION AI772648
VERSION AI772648.1 GI:5270689
KEYWORDS EST
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 527)
D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nierman,M., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>

TITLE
JOURNAL
COMMENT

FEATURES
source
5 prime sequence.
Location/Qualifiers
1. .527
/organism="Lycopersicon esculentum"
/cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="CLER312"
/clone_lib="tomato resistant, Cornell"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2: XhoI; CLER - tomato Pseudomonas Resistant EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT 155 a 104 c 133 g 135 t
ORIGIN

Query Match 31.0%; Score 126.4; DB 10; Length 527;
Best Local Similarity 62.8%; Pred. No. 2.5e-25;
Matches 196; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 96 atgaagatcccaagtgatcgtcgtcgaagaagaagaagaacatacttca 155
Db 15 ATGAAGTACAAATCCAGAGATCTCTCCGCGGAAGAGCAGGCTCATTTACG 74
Qy 156 gcaccatctctgtagcagaatactcagtagtcaccctgtccaaaggaactcag 215
Db 75 GCGCCTTCAAGTGGCGCGCGATTTTAATGAGCGCACCTTATGTCGAGTTACGTGA 134
Qy 216 aaatacagcgttcgtcttaccatcgaagaagaagaagaatcatagtcgcgga 275
Db 135 AAGTACACGTAAGATCTATGCCGTGAGAAAGATGACGAAGTTGTCGTTGCGGA 194
Qy 276 gcttcaaggtagaagaagaagaatcacaacgtgtatcgaagaagaatcagatcat 335
Db 195 ACTTACAAAGGCGCGTACGAGGAAGTTGTTCAAGTGTACCTAAGAAATGGTGATCCAC 254
Qy 336 atcgagaagtagcagcagaagaagaagaatgaatgaatgaatgaatgaatcaca 395
Db 255 ATTGAACGTATACACGAGAGAGTCATGATCTACTGTGAACGTTGGATTCATCCT 314
Qy 396 tctaattggt 407
Db 315 TCGAAGTTGTT 326

Search completed: March 2, 2002, 20:28:49
Job time: 1519 sec

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